Mechanisms contributing to synaptic Ca²⁺ signals and their heterogeneity in hair cells

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Sound coding at hair cell ribbon synapses is tightly regulated by Ca2+. Here, we used patch-clamp, fast confocal Ca2+ imaging and modeling to characterize synaptic Ca2+ signaling in cochlear inner hair cells (IHCs) of hearing mice. Submicrometer fluorescence hotspots built up and collapsed at the base of IHCs within a few milliseconds of stimulus onset and cessation. They most likely represented Ca2+ microdomains arising from synaptic Ca2+ influx through Ca_V1.3 channels. Synaptic Ca²⁺ microdomains varied substantially in amplitude and voltage dependence even within single IHCs. Testing putative mechanisms for the heterogeneity of Ca²⁺ signaling, we found the amplitude variability unchanged when blocking mitochondrial Ca2+ uptake or Ca2+-induced Ca2+ release, buffering cytosolic Ca²⁺ by millimolar concentrations of EGTA, or elevating the Ca2+ channel open probability by the dihydropyridine agonist BayK8644. However, we observed substantial variability also for the fluorescence of immunolabeled Ca_V1.3 Ca²⁺ channel clusters. Moreover, the Ca2+ microdomain amplitude correlated positively with the size of the corresponding synaptic ribbon. Ribbon size, previously suggested to scale with the number of synaptic Ca²⁺ channels, was approximated by using fluorescent peptide labeling. We propose that IHCs adjust the number and the gating of Cav1.3 channels at their active zones to diversify their transmitter release rates.

calcium microdomain | coding | imaging | ribbon synapse | modeling

air cells transform mechanical stimuli into glutamate release at their ribbon-type synapses (reviewed in refs. 1 and 2). This involves a tight regulation of synaptic vesicle exocytosis by Ca²⁺ channels (3–7), which are of Ca_V1.3 type (8). The Ca²⁺ channels cluster at the multiple active zones of hair cells (5, 9–14). Imaging of Ca²⁺ indicator fluorescence has revealed localized microdomains of elevated [Ca²⁺] in lower vertebrate hair cells (10–12, 14), whereas a spatially less confined rise of submembrane [Ca²⁺] involving Ca²⁺-induced Ca²⁺ release (CICR) has been reported for immature mouse inner hair cells (IHCs) (15).

Our understanding of sound encoding in the mammalian cochlea is partly limited by a lack of quantitative information on synaptic Ca²⁺ signaling in the IHCs of hearing animals. For example, it is believed that differences between the synapses of an individual IHC account for the variability of spontaneous and evoked rates, sound threshold, and dynamic range among spiral ganglion neurons (SGNs) of similar characteristic frequency (16). Presynaptic and postsynaptic mechanisms have been suggested to cause this heterogeneity of SGN dynamics. Differential efferent control of SGN activity (17) seems conceptually obvious. There are also indications for differences in structure (18) and function (19) among active zones of an IHC; however, little is known about the underlying mechanism. Here, we used time-resolved confocal imaging of the fluorescence of low-affinity Ca²⁺ indicators together with pharmacological manipulations and modeling to characterize synaptic Ca²⁺ microdomains in IHCs of hearing mice.

Results

Fast and Localized Ca²⁺ Signals Mediated by Ca²⁺ Influx at IHC Active **Zones.** Voltage activation of Ca²⁺ influx caused the appearance of submicrometer fluorescence hotspots in the basolateral compartment of IHCs ($[Ca^{2+}]_e = 5 \text{ mM}$; Fig. 1A) that had been filled with the low-affinity Ca²⁺ indicator Fluo-5N (400 μ M, $K_d = 95$ μ M; M. Alp and W. M. Roberts, personal communication) and the slow Ca^{2+} chelator EGTA (2 mM, $K_d = 180$ nM at pH 7.2) (20). These conditions ("standard conditions") favored detection of localized Ca²⁺ signals by augmenting Ca²⁺ influx (elevated [Ca²⁺]_e) and limiting intracellular Ca²⁺ spread (EGTA, e.g., ref. 14). The low affinity of Fluo-5N led us to primarily display fluorescence changes $(F - F_0 \text{ or } \Delta F)$ without background normalization (avoiding an increase in noise due to division by low F_0). In contrast to reports regarding other ribbon synapses (10), we did not observe obvious spot-like Ca²⁺ indicator fluorescence at rest, arguing against a notable association of the indicator with ribbons. The Ca²⁺ indicator fluorescence hotspots (spanning hundreds of nanometers) are further on referred to as Ca²⁺ microdomains to distinguish them from Ca²⁺ nanodomains, which are implied for Ca²⁺ signals that operate within a few tens of nanometers of the source and have escaped visualization because of the limited spatial resolution of conventional light microscopes (21).

The Ca²⁺ microdomains colocalized with synaptic active zones, shown by marking the synaptic ribbons with a rhodamine-conjugated CtBP2/RIBEYE-binding peptide (Fig. 1*B*) (22). We did not observe CtBP2/RIBEYE-marked spots without Ca²⁺ microdomains. We searched for Ca²⁺ microdomains in stacks of confocal sections from the base to the apex of the IHC that were acquired during repetitive depolarization. The number of Ca²⁺ microdomains (8 \pm 2 per IHC, n = 4 IHCs) was consistent with typical observations of labeled ribbons (e.g., Figs. 1*B Left* and 5*B*). Neither Ca²⁺ microdomains nor ribbons were observed apical to the nucleus. Ca²⁺ microdomains could not be elicited in the absence of extracellular Ca²⁺ (Fig. 1*C*, representative for n = 3 IHCs).

The spatiotemporal properties and voltage dependence of synaptic Ca^{2+} microdomains were studied at high temporal resolution by using "spot detection" (23) and line scanning. For spot detection, we positioned the laser beam on the brightest pixel in a Ca^{2+} microdomain of the previously acquired xy-scan (white spot in the center of the Ca^{2+} microdomain of Fig. 24) and recorded the fluorescence at an effective rate of ≈ 2 kHz (*Methods*). Note that we visually chose the best focal plane, routinely performed spot detection at 7 locations in a line (standard method; white spots in Fig. 2A, enabling isochronal

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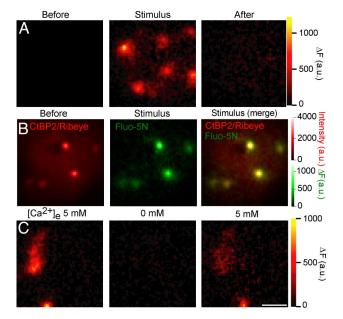


Fig. 1. Ca²⁺ microdomains mediated by Ca²⁺ influx at ribbon synapses in IHCs. Confocal images of Fluo-5N-filled IHCs were acquired in 3 repetitions of 6 images at \approx 10 Hz: 2 images each before, during, and after stimulation by 200-ms depolarizations to -7 mV. Images averaged over runs and time frame (e.g., before stimulation) are shown. (A) Representative series of images under standard conditions showing 6 Fluo-5N fluorescence hotspots (Ca²⁺ microdomains) during the stimulus. The images were baseline subtracted (subtracting the average of the 2 images before depolarization; ΔF). On display are the image during stimulation and those preceding or following the stimulus. (B) Ca²⁺ microdomains (Center) evolved at ribbon synapses marked by rhodamineconjugated CtBP2/RIBEYE-binding peptide (40 μ M; Left, acquired before stimulation). Overlay (Right) depicts colocalization of Ca²⁺ microdomains and synaptic ribbons (both fluorescence channels acquired simultaneously). Note the extension of Ca²⁺ microdomains beyond ribbons. For 2-dye imaging, acquisition was repeated 6 instead of 3 times. (C) Ca²⁺ microdomains were abolished by omission of extracellular Ca²⁺ (Center, bath perfusion of nominally Ca²⁺-free solution and addition of 1 mM EGTA and 5 mM MgCl₂) and reappeared after readdition of 5 mM [Ca²⁺]_e to the IHC (imaging as in A). (Scale bars: 2 μ m.)

analysis: Fig. 2C) and chose the position with the largest ΔF for further analysis.

Fig. 2 B-D illustrates the rapid build-up and collapse of Fluo-5N fluorescence upon stimulus onset and cessation. We note that the presented kinetics of ΔF underestimate the true speed of the [Ca²⁺] change because of the limiting binding kinetics of the Ca²⁺ indicator as well as spatial averaging in the process of detection [supporting information (SI) Fig. S1d and SI Text (23). The kinetics were quantified by single- or doubleexponential fitting (Fig. 2B and Table S1). Moving the excitation detection volume outside the center of a given Ca²⁺ microdomain revealed a reduction of ΔF and progressive slowing of onset and offset kinetics (Fig. 2 B and C). Note the pronounced amplitude variability of ΔF (Fig. 2D). The distribution of maximal ΔF values [ΔF_{max} , peak fluorescence identified after boxcar (2-ms box) smoothing had a coefficient of variation (CV) of 0.74 (45 Ca²⁺ microdomains in 17 IHCs). Similar variance was observed in the background-normalized data ($\Delta F/F_0$, CV = 0.65; Fig. S2a) and for the ΔF_{max} distribution estimated by fitting Gaussian functions to time-averaged line scans (CV = 0.75, 35Ca²⁺ microdomains in 17 IHCs). We observed a trend toward smaller variance with more precise colocalization of beam position and Ca²⁺ microdomain center (SI Text), probably reflecting the contribution of measurement variance. Therefore, we consider the most accurate approach (3D spot displacement) to yield the most reliable estimate of ΔF_{max} variability (CV =

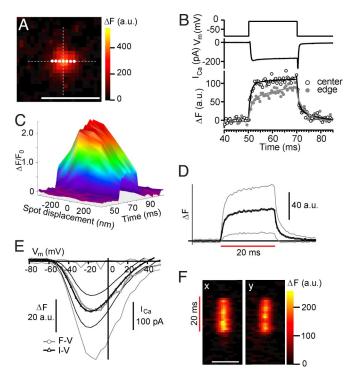
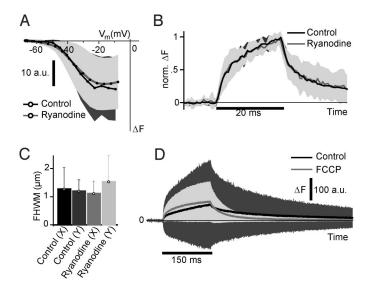


Fig. 2. Spatiotemporal properties and voltage dependence of Ca²⁺ microdomains. (A) Confocal image of a Ca²⁺ microdomain illustrating read-out sites for spot detection (white spots) and line scans (orthogonal dashed lines). (Scale bar: 2 μ m.) (B) Representative spot detection experiment: the laser spot was first placed on the brightest pixel in the xy confocal image (A, center white spot). Top of the graph shows voltage protocol, middle shows Ca²⁺ current, and bottom shows ΔF at the center spot (black) and an outlying position (260 nm off center, gray). Ca²⁺ current (I_{Ca}) and ΔF represent averages obtained from 5 subsequent runs (interval: 2.25 s). Lines represent exponential fits to the ΔF rise and decay. (C) Isochronal analysis: the laser spot was subsequently displaced bilaterally from the center, and the fluorescence was recorded as described in B. ΔF traces were assembled in a pseudo-3D plot as a function of time and space. (D) Mean (black) and SD (gray) of 45 Ca²⁺ microdomains (in 17 IHCs) recorded as described in B; note the large amplitude variability. For each Ca²⁺ microdomain, only the maximum intensity recording was considered. (E) Mean and SD of ΔF (gray) as a function of depolarizing potential (V_m), obtained from spot-detection experiments at the center of the Ca²⁺ microdomain ($n = 32 \text{ Ca}^{2+}$ microdomains in 17 IHCs); ΔF was averaged over the last 15 ms of a 20-ms stimulus. ΔF (mean: gray) and I_{Ca} (mean: black) show a similar voltage dependence (thin lines: corresponding SDs). (F) Representative line scans (x and y, corresponding to the x and y scan lines in A). Red bar indicates time of depolarization to -7 mV. (Scale bar: 2 μ m.)

0.54). However, when using this more extensive search, one trades more accuracy in beam position for more rundown of Ca²⁺ influx and risk of photodamage. Hence, we did not generally apply 3D spot displacement, but used the standard method for most experiments (unless stated otherwise).

Variability of ΔF_{max} was only slightly smaller within individual IHCs (Fig. S2 b-d and SI Text), indicating that intracellular variability dominates the variance of the entire population of Ca²⁺ microdomains. Thus, we interpret the population estimates to indicate intracellular variability throughout. Based on our in situ $F_{\text{max}}/F_{\text{min}}$ ratio (\approx 50) and noting the limitations inherent to [Ca²⁺] quantification using nonratiometric indicators, we estimated the average [Ca²⁺] within the Ca²⁺ microdomain to be ≈ 3 μM at the end of a 20-ms depolarization (standard conditions). The voltage dependence of ΔF qualitatively mimicked that of the simultaneously acquired Ca²⁺ current, further indicating that ΔF reflects synaptic Ca^{2+} influx (Fig. 2E). The spatial distribution of the Ca²⁺ signals was quantified by 2 orthogonal line scans (Fig. 2F, lines indicated in Fig. 2A). Following the Ca^{2+} microdo-



Blocking CICR or mitochondrial Ca²⁺uptake. (A) Comparable mean (line) and SD (shaded area) of ΔF vs. membrane voltage ($V_{\rm m}$) for cells loaded with either 100 μ M ryanodine (12 microdomains in 9 IHCs) or vehicle (16 microdomains in 13 IHCs) via the patch pipette (KCl-based solution with 0.5 mM EGTA; see Methods). ΔF was obtained by spot detection as described in Fig. 2E. For each microdomain, the voltage protocol was repeated 3 times. $V_{\rm m}$ was offline-corrected for the voltage drop over residual series resistance, which was very relevant here because of the remaining potassium current. (B) Similar onset and decay kinetics with (gray, 15 microdomains in 10 IHCs) and without (black, 19 microdomains in 14 IHCs) ryanodine. Average (line) and SD (shaded area) of normalized ΔF traces (spot detection following depolarization to "nominally" -15.3 mV; only recordings with a voltage error <4 mV were considered). (C) Mean and SD of the FWHM of the Ca2+ microdomain along both perpendicular scan lines (fitting of a Gaussian function to the average of all lines acquired during depolarization). No difference was found between the 2 groups. X (control): 11 Ca2+ microdomains in 10 IHCs, Y (control): 7 Ca²⁺ microdomains in 7 IHCs, X (ryanodine): 11 Ca²⁺ microdomains in 8 IHCs, and Y (ryanodine): 8 Ca²⁺ microdomains in 6 IHCs). (D) Mean and SD of ΔF traces recorded by spot detection in response to 150-ms depolarizations to -7 mV (0.5 mM EGTA and 375 μ M Fluo-4FF in the pipette; 10 mM [Ca²⁺]_e and 5 μ M BayK8644 in the bath) in control experiments (n=11 Ca²⁺ microdomains in 7 IHCs), and in intracellular presence of FCCP (10 μ M) and oligomycin (2.5 mg/mL), blocking mitochondrial Ca^{2+} uptake ($n = 23 Ca^{2+}$ microdomains in 10 IHCs).

main build-up during the first 1–2 ms, there was little spatial spread during the course of the depolarization under standard conditions.

Exploring the Mechanisms Underlying the Ca²⁺ Microdomain Heterogeneity. What differentiates the Ca^{2+} signals between synapses of a given IHC? Possible mechanisms include disparities in Ca^{2+} release from intracellular stores (e.g., CICR), Ca^{2+} buffering, and/or Ca^{2+} sequestration. Moreover, and most importantly, there could be differences in any of the 3 determinants of Ca^{2+} influx: number of channels, open probability, and single-channel current.

CICR mediated by ryanodine receptors could amplify a Ca^{2+} influx-mediated $[Ca^{2+}]$ rise to various degrees. We tested for a potential contribution of CICR to presynaptic Ca^{2+} signals by comparing the spatiotemporal properties and the voltage dependence of the Ca^{2+} microdomains elicited by 20-ms depolarizations in the presence or absence of a ryanodine receptor antagonist (100 μ M ryanodine in the pipette, Fig. 3 A–C; 20 or 40 μ M ryanodine in the bath, Fig. S3). To favor the detection of a small CICR contribution, we entailed weaker cytosolic Ca^{2+} buffering (0.5 mM EGTA). None of these conditions caused a significant change in ΔF (Fig. 3A and Table S1), the rise and

decay kinetics (Fig. 3B), spatial distribution (Fig. 3C), the voltage of half-maximal ΔF activation, or the variability of $\Delta F_{\rm max}$ (Tables S1 and S2). These results are consistent with observing comparable amplitudes and amplitude scatter, regardless of whether K⁺ or Cs⁺ [which blocks CICR (15)] was used as the main intracellular cation. In summary, we conclude that CICR does not contribute significantly to synaptic Ca²⁺ signaling in mature IHCs and cannot explain the observed synaptic heterogeneity.

Synaptic Ca²⁺ removal may differ across IHC active zones. Ca²⁺ may be cleared temporarily by mitochondria (24) or bind to immobile cytosolic Ca2+ binding sites (25, 26). For sensitive detection of Ca²⁺ changes due to mitochondrial Ca²⁺ uptake, we used a Ca^{2+} indicator with higher affinity (Fluo-4FF, 375 μ M, $K_{\rm d} = 10 \ \mu \rm M$; M. Alp and W. M. Roberts, personal communication) and weak cytosolic Ca²⁺ buffering (0.5 mM EGTA). Under these conditions, blocking mitochondrial Ca²⁺ uptake by intracellular carbonyl cyanide 4-(trifluoromethoxy)phenylhydrazone (FCCP, $10 \mu M$, coapplied with oligomycin, 2.5 mg/mL) did not alter the Ca²⁺ microdomains, except for making the slow component of the fluorescence rise slightly faster (Fig. 3D and Table S1). Moreover, the CVs of the Ca²⁺ microdomain amplitudes were in the same range (1.06 vs. 0.91 for control and FCCP, respectively), arguing against a prominent contribution of variable mitochondrial Ca²⁺ uptake to heterogeneity of synaptic Ca²⁺ signals.

Addition of EGTA (0.5, 2, and 10 mM) to the pipette solution was used to study the effects of mobile Ca²⁺ buffers on the spatiotemporal properties of Ca²⁺ microdomains and their heterogeneity in 5 mM [Ca²⁺]_e. For comparison, we performed experiments under close to physiological conditions ("native" Ca²⁺ buffering, perforated-patch configuration, physiological [Ca²⁺]_e: 1.3 mM). For dye loading, the perforated-patch recordings were preceded by a brief whole-cell episode (15–30 s, 2 mM [Fluo-5N]_{pipette}), avoiding major loss of cellular Ca²⁺-buffering proteins (SI Text).

Spots were identified in each condition, but were of smaller amplitude and spatially more confined with higher Ca²⁺ buffering capacity (Fig. 4A-C and E). The rise and decay kinetics as well as the spatial distribution of Ca²⁺ microdomains observed in perforated-patch experiments were most similar to those found with 0.5 mM EGTA. To quantitatively characterize activezone Ca²⁺ dynamics in the well-defined whole-cell experiments, we compared the experimental data to predictions of a model of Ca²⁺ influx, diffusion, and binding by using CalC software (27) and simulating Ca²⁺ indicator fluorescence detection (for details, see Fig. S1, *SI Text*, and Table S3). Mobile endogenous Ca²⁺ binding sites, which are progressively "washed out" into the pipette in the whole-cell configuration, were disregarded, as were mitochondrial Ca²⁺ uptake and CICR. ΔF was predicted by transforming the spatiotemporal distribution of Ca²⁺-bound Fluo-5N by our in situ $F_{\text{max}}/F_{\text{min}}$ ratio (\approx 50), as described (28), and convolution with the point spread function of the optical setup. The model predicted the mean properties of the fluorescent hotspots under the different conditions reasonably well (Fig. 4 C–E).

Experiments and model consistently showed biexponential rise and decay kinetics in weak exogenous buffering conditions, whereas the slow components were strongly diminished by increasing EGTA (Fig. 4D and Table S1). In addition, high EGTA accelerated the fast Ca²⁺ decay (Fig. 4D and Table S1). The widths of the Ca²⁺ microdomains in different EGTA concentrations were well predicted by the model (Fig. 4E). The width of the Ca²⁺ microdomains increased throughout the depolarization (20 ms) for lower concentrations, but it rapidly reached steady state with EGTA 2 mM or greater (Fig. S4). The choice of the Ca²⁺-buffering condition did not appreciably affect the experimentally observed synaptic heterogeneity for any of the quantified parameters (Fig. 4B and Table S1). Finding

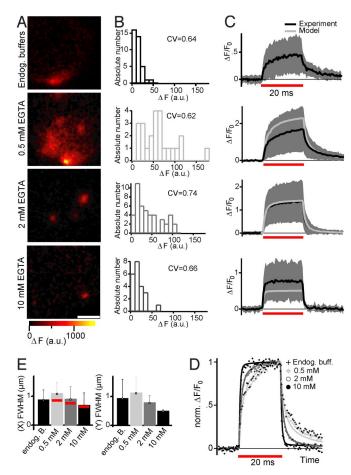
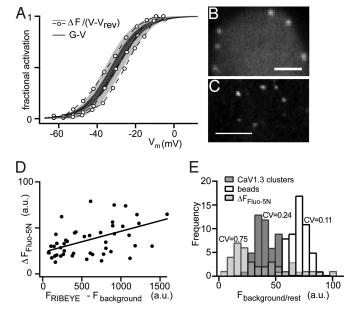


Fig. 4. Effects of Ca²⁺ buffering on IHC Ca²⁺ microdomains. (A) Representative confocal ΔF images of IHCs (recorded as introduced in Fig. 1 A) with close to native endogenous Ca2+ buffering (perforated-patch, top row, representing 37 Ca²⁺ microdomains in 14 IHCs) or various amounts of exogenously added EGTA: 0.5 mM (second row, representing 24 Ca²⁺ microdomains in 15 IHCs), 2 mM (third row, representing 45 Ca²⁺ microdomains in 17 IHCs), or 10 mM (bottom row, representing 22 Ca²⁺ microdomains in 7 IHCs). (Scale bar: 2 μ m.) (B) Distributions of $\Delta F_{\rm max}$ obtained for the buffering conditions in spot-detection experiments after box-car smoothing (2-ms box). (C) Experimental mean (black line) and SD (gray area) of $\Delta F/F_0$ traces as well as model prediction (gray line) for the respective buffering conditions. Model predictions were obtained only for exogenous buffering experiments (see Table S1 and SI Text) (D) Normalized mean $\Delta F/F_0$ traces of all 4 buffering conditions (markers) emphasizing the kinetic differences, and model predictions (lines) for exogenous buffering experiments. (E) Mean and SD of FWHM of the Ca²⁺ microdomain along both scan lines (fitting of a Gaussian function to the time-averaged line profile). Also shown are the model predictions (red bars).

comparable synaptic heterogeneity with an excess of mobile Ca²⁺ buffer renders differences in local Ca²⁺ buffering unlikely to contribute substantially.

Heterogeneity of Ca²⁺ influx is an attractive candidate mechanism, under direct control of the membrane potential. Indeed, we observed substantial variability in the voltage dependence of ΔF across the Ca²⁺ microdomains (Fig. 5A), even within a given IHC (dotted lines in Fig. 5A), which probably reflected differences in gating. The variance of the voltage of half-maximal activation was larger for the Ca2+ microdomains (24 mV2; standard conditions, see Table S1 for other conditions) than for the Ca²⁺ current in the corresponding IHCs (5 mV²). Voltage errors due to changes in electrode potential were found to be less than 3 mV, and series resistance-related errors were corrected offline.

However, substantial ΔF variability was observed also for



Heterogeneous voltage dependence and Ca²⁺ channel number of synaptic Ca²⁺ channel clusters in IHCs. (A) To demonstrate the variable voltage dependence of ΔF_{max} , we display the average results (and SD) of fitting a Boltzmann function to the fractional voltage activation of ΔF [ΔF divided by the driving force $(V - V_{rev})$ of the underlying Ca²⁺ current]. Note that at -7mV, the potential used for comparisons in Figs. 2 D and F, 3 B-D, 4, and 5 D and E, the activation of ΔF (mean: gray line, SD: light gray area) and I_{Ca} (mean: black line, SD: dark gray area) is nearly complete. Note the pronounced variability in the voltage dependence of activation, even within 1 cell (dashed traces: individual data curves from 3 Ca²⁺ microdomains in an IHC). (B) shows an xy scan through the basal portion of an IHC loaded with rhodamine-conjugated, CtBP2/RIBEYE-binding peptide (40 μ M; dissolved in intracellular solution). Note the spots of increased fluorescence intensity, indicative of synaptic ribbons. (Scale bar: 2 μ m.) (C) Representative confocal section of an IHC stained with a $Ca_V1.3$ antibody. (Scale bar: 2 μ m.) (D) Correlation between Ca^{2+} microdomain ΔF_{max} and fluorescence intensity of the corresponding ribbon (amplitude of 2D Gaussian function, fit to the fluorescently tagged ribbon in xy scans acquired at rest and before spot detection). The microdomain ΔF_{max} was obtained at the maximum-intensity location, identified by a series of 11 axially (along optical axis) displaced measurements (200-nm steps). Note the positive correlation ($P_r = 0.47$, P < 0.01; $n = 48 F_{Ca} - F_{RIBEYE}$ pairs in 18 IHCs). (E) Distributions of Ca²⁺ microdomain ΔF_{max} (amplitude of 1D Gaussian fit to time-averaged line-scan profile, n = 35), Ca_V1.3 immunofluorescence (n = 50), and 210-nm crimson bead fluorescence (n = 52).

saturating stimuli (at -7 mV: Fig. 5A; see Figs. 2, 4, and 5 for illustration). Next, we tested whether the dihydropyridine L-type channel agonist BayK8644 (29) could reduce the ΔF heterogeneity of the Ca²⁺ microdomains. By uniformly increasing the open probability of Cav1.3 channels in IHCs (5), we reasoned that BayK8644 would equalize stimulus-dependent Ca²⁺ influx between IHC active zones. To prevent local Ca²⁺ saturation of Fluo-5N, we added a high concentration of EGTA (10 mM in the pipette, shown above to not reduce heterogeneity of ΔF). However, despite the maximized open probability, we still found large variability in ΔF (CV = 0.87, 16 Ca²⁺ microdomains in 5 IHCs) (Table S1).

The Ca²⁺ channel number per active zone has been suggested to vary with the size of the synaptic ribbon in hair cells in chick, frog, and turtle hair cells (30). This was based on a correlation of the estimates of Ca²⁺ channel number and of total release area (product of synapse number and ribbon size) per hair cell. Here, we explored this hypothesis at the single-synapse level and asked whether differences in channel number could contribute to the heterogeneity of Ca²⁺ microdomain amplitudes. We related the Ca^{2+} microdomain amplitude (Fluo-5N ΔF , spot detection,

20-ms depolarizations to -7 mV) to the fluorescence intensity of the corresponding peptide-labeled ribbons before depolarization (Fig. 1B and 5B). Ribbon fluorescence intensity (amplitude of 2D Gaussian function fit) rather than FWHM was used for approximation of ribbon size, because ribbons are too small to be faithfully measured by confocal microscopy (31). Relating the fluorescence intensity to ribbon size seems reasonable, as previous work (22) indicated a quantitative scaling of ribbon labeling by the fluorescent CtBP2/RIBEYE-binding peptide with the number of contained RIBEYE molecules. As shown in Fig. 5D, we did observe a significant correlation between Ca²⁺ microdomain amplitude and the ribbon fluorescence intensity. This suggests that larger Ca²⁺ microdomain amplitudes arose from bigger active zones, probably containing more Ca²⁺ channels, and that differences in Ca²⁺ channel number among synapses can account for part of the variance of their Ca² microdomain amplitudes.

The attractive hypothesis of a variable Ca²⁺ channel content was tested by confocal microscopy of active zones following Ca_V1.3 immunolabeling (Fig. 5C). We estimated the fluorescence intensity as described above for ribbons. Images were acquired using a low numerical aperture (0.7) objective lens to ensure that most of the Ca_V1.3 immunofluorescent spot was included in the excitation-detection volume. We reasoned that active zones with larger Ca²⁺ channel clusters or clusters with higher Ca²⁺ channel densities would display higher fluorescence intensities (assuming a linear labeling reaction). The measurement revealed considerable variance among the synapses (CV = 0.24; Fig. 5E). We also measured fluorescent beads using the same microscope and detection settings (diameter 210 nm; Fig. 5E) to get an upper boundary of the imaging- and analysis-related contributions (CV = 0.11). For comparison, Fig. 5E also displays the fluorescence intensity distribution of Fluo-5N hotspots.

Discussion

Toward a Quantitative Understanding of the Active-Zone Ca²⁺ Microdomain in IHCs. Studying IHCs of mice after the onset of hearing (low-affinity Ca²⁺ indicator, 0.5–10 mM EGTA), we observed spatially confined Ca2+ domains much like those reported for lower vertebrate hair cells (10-12, 14). Based on our experiments, localized domains of high Ca²⁺ concentration are likely to occur at IHC synapses with physiological Ca²⁺ influx and native Ca²⁺ buffering. Several lines of evidence suggest that the observed Ca2+ microdomains arose from Ca2+ influx through synaptic Ca_V1.3 Ca²⁺ channel clusters at the ribbon synapses. First, they occurred at sites marked by a ribbonlabeling, CtBP2/RIBEYE-binding, fluorescent peptide, and their number was consistent with counts of ribbon synapses (this study, and ref. 31). This argues against an appreciable fraction of presynaptically silent synapses as well as against Ca2+ microdomains occurring outside ribbon-type active zones. Second, Ca²⁺ microdomains were not observed when removing extracellular Ca²⁺. Third, their amplitude shared the voltage dependence of the whole-cell Ca2+ current. Fourth, inhibition of CICR by ryanodine or intracellular Cs+ did not reduce the amplitude of the Ca²⁺ microdomains. Finally, the fluorescence changes could be reasonably well predicted by realistic modeling of active-zone Ca²⁺ signals, driven solely by Ca²⁺ influx, without invoking additional Ca²⁺ sources.

Experiments with different EGTA concentrations and modeling were used to explore how mobile Ca^{2+} buffering shapes the spatiotemporal properties of the Ca^{2+} microdomains. In brief, the more mobile Ca^{2+} binding sites were present, the faster, smaller, and spatially more constrained were the observed and simulated Ca^{2+} changes. This can be intuitively understood to reflect a faster Ca^{2+} capturing and less Ca^{2+} buffer saturation. Mobile Ca^{2+} buffering presented the prevailing Ca^{2+} removal

mechanism, limiting the active zone's Ca²⁺ signal of IHCs in space and time during short depolarizations. This agrees well with conclusions of previous studies on other hair cells (11, 12).

Heterogeneity of Synaptic Ca²⁺ Signals: Mechanisms and Consequences. The voltage dependence varies even among active zones of an individual IHC, which may relate to the observation of different stimulus thresholds for styryl dye destaining across putative ribbon synapses (19). Because the hair cell is isopotential (9), voltage errors due to series resistance were corrected, and those due to drifts in electrode potential were minor, we expect experimental procedures to contribute little to the observed variance of the voltage of half activation (24 mV²), which was 4 times larger than that of the whole-cell current compared among the same experiments.

Besides shifts in activation curves, we also found a large $\Delta F_{\rm max}$ variability of Ca²⁺ microdomains for strong depolarizations (-7 mV) when Ca²⁺ channel activation saturates and even after maximization of channel open probability by BayK8644. Although some contribution of the measurement to the observed variance of Ca²⁺ microdomain amplitude is likely, this indicates variability of Ca²⁺ signaling in addition to that arising from differences in voltage gating (discussed above). Our data do not support a major contribution of Ca²⁺ signal amplification by CICR, local differences in Ca²⁺ buffering/sequestration, or the average maximal Ca²⁺ channel open probability among IHC synapses.

Heterogeneity in the number of Ca²⁺ channels among hair cell active zones could explain a substantial part of the observed amplitude variability of Ca²⁺ microdomains at saturating depolarizations. Confocal microscopy of immunolabeled Cav1.3 channel clusters indicates that the number of Ca2+ channels indeed varies among hair cell synapses (CV = 0.24; Fig. 5). This result was obtained from measurements on fixed tissue, and therefore not from those synapses that had been functionally characterized. However, the argument is supported by the simultaneous imaging of Ca²⁺ microdomains and their corresponding, fluorescently labeled ribbons. The observed positive correlation of both fluorescence intensities suggests that larger Ca²⁺ microdomains arise from active zones with more Ca²⁺ channels. This hypothesis assumes that (i) the fluorescence of the peptide-labeled ribbon indicates the number of RIBEYE molecules (22) and (ii) can be used to approximate ribbon size, (iii) which scales with the spatial extent of the active zone and the number of Ca²⁺ channels (30). Modeling confirmed that under our experimental conditions, the contributions of individual Ca²⁺ channels at the active zone sum roughly linearly to set the amplitude of the Ca²⁺ microdomain reported by the low-affinity indicator Fluo-5N and our imaging system (Fig. S1e and SI Text). Whether the remaining mismatch of amplitude variance between Ca²⁺ microdomain and Ca_V1.3 channel immunofluorescence reflects differences in Ca²⁺ channel regulation among synapses remains to be addressed in future studies.

In summary, we propose that the IHC adjusts both the number of Ca²⁺ channels and their gating at its individual synapses. This could explain the coexistence of synapses within an individual hair cell that drive different SGN firing rates. Transmitter release from IHCs seems to be controlled by Ca²⁺ nanodomains around Ca²⁺ channels within few tens of nanometers of the docked vesicle (2, 5, 7, 32). In this case, the number of open channels would relate linearly to the rate of vesicle exocytosis. This concept has been primarily tested for fusion of the readily releasable pool of vesicles (5, 7), but probably also applies during longer stimuli (6). Differences in the number of channels opening for given receptor potential amplitude would translate into different peak and adapted firing rates. However, synapses with more Ca²⁺ channels and/or a more negative voltage range of channel activation would also cause higher spontaneous firing rates, which in SGNs seem entirely driven by hair cell transmitter release (33). The question of how these

properties are differentially regulated in a single IHC remains to be addressed in future studies.

Methods

Animals. C57BL/6 mice (ages 14-18 days) were used for experiments.

Patch-Clamp and Confocal Ca2+ Imaging. IHCs from apical coils of freshly dissected organs of Corti were patch-clamped as described previously (4). The pipette solution contained (in mM): 130 cesium glutamate, 13 tetraethylammonium (TEA)-Cl, 20 CsOH–Hepes, and 1 MgCl $_2$, and 250 μ g/mL amphotericin B (pH7.2) for perforated-patch recordings, in addition to (in mM) 2 MgATP, 0.3 NaGTP, and various concentrations of EGTA (standard: 2 mM; cesium glutamate concentration adjusted for 10 mM EGTA), 0.4 mM Fluo-5N or 0.375 mM Fluo-4FF (penta-K⁺ salts; Invitrogen) (pH 7.0) for standard whole-cell recordings, and for CICR experiments (in mM): 155 KCl, 20 KOH-Hepes, 2 MgATP, and 0.3 NaGTP (pH 7.0). The extracellular solution contained (in mM: if deviating. concentrations used for CICR experiments are given in brackets): 102 [133] NaCl, 35 [3] TEA-Cl, 2.8 [5.8] KCl, 5 CaCl₂ (1.3 for perforated-patch recordings; balanced by NaCl), 1 MgCl₂, 10 NaOH-Hepes, and 10 D-glucose (pH 7.3). BayK8644 (5 μ M; Tocris) was bath applied. Ryanodine (Calbiochem) was either dissolved in the pipette solution (100 μ M) or continuously bath applied (20 or 40 μ M). FCCP (10 μ M; Fluka) and oligomycin (2.5 mg/mL; Sigma) were intracellularly applied. An EPC-9 amplifier and Patchmaster software (HEKA Elektronik) were used for measurements. All voltages were corrected for liquid-junction potentials (17.5 mV for cesium glutamate solution and 5.3 mV for KCl solution) and voltage drops across series resistance. Currents were low-pass-filtered at 5 kHz and sampled at 50 kHz. Cells with a membrane current exceeding -50 pA at our standard holding potential of -87.5 mV (cesium glutamate; for KCl solution, -75.3 mV) were discarded from analysis. Ca²⁺ currents were further isolated from background current by using a P/n protocol. Current-voltage relationships were fitted by using a Boltzmann function. Interstimulus periods were 2–3 s between sweeps and 1–2 min between ensembles. The average Ca²⁺ current rundown at the end of the experiment was 30% of the maximum current.

Ca²⁺ imaging was performed with a Fluoview 300 confocal scanner mounted on an upright microscope (BX50WI) equipped with a 0.9 numerical aperture, 60× water-immersion objective (all from Olympus). A 50-mW, 488-nm laser (Cyan; Newport Spectraphysics) was used for excitation of Fluo-5N, and a 1.5-mW, 543-nm He-Ne laser was used for excitation of rhodamineconjugated, CtBP2/RIBEYE-binding peptide. Ca2+ microdomains were identi-

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fied in xy scans during 200-ms depolarizations [0.5% of maximum laser intensity (488 nm)] and were further characterized by using spot detection and line scans. During spot detection [0.05% of maximum laser intensity (488 nm)], the output of the photomultiplier tube (PMT) signal (500 kHz) was temporally averaged to yield an effective sampling rate of 1.85 kHz. Line scans were acquired at a rate of 0.74 kHz [0.25% of max laser intensity (488 nm)]. Isochronal spot detection measurements and line scans were repeated 5 and 10 times, respectively. For 2-dye imaging, the laser intensities (488 nm) were doubled. The 543-nm laser was operated at the following intensities: 50% for xy scans, 25% for line scans, and 10% for spot detection. PMT dark current was subtracted for all measurements, and PMT settings were identical for all experiments. In rare cases, we observed an unclear long-term rise in fluorescence that was independent of leak current amplitude.

Immunohistochemistry. The freshly dissected apical cochlear turns were fixed for 25 min in 99% methanol at -20°C. Immunostaining was performed as described in ref. 31. The following antibodies were used: mouse IgG1 anti-CtBP2 (also recognizing the ribbon protein RIBEYE; 1:150; BD Biosciences), rabbit-anti-Ca_V1.3 (1:75; Alomone Labs), and secondary AlexaFluor488labeled and AlexaFluor568-labeled antibodies (1:200: Molecular Probes). Confocal images of Ca_V1.3-immunolabeled IHCs were acquired by using an SP5 confocal microscope (Leica) with 488-nm (Ar) and 561-nm (DPSS) lasers for excitation and a $63 \times$ oil immersion objective (numerical aperture 0.7).

Model and Data Analysis. Fig. S1, SI Text, and Table S3 provide a detailed description of the model using CalC (http://web.njit.edu/~matveev/calc.html). Data are presented as mean and SD. Igor Pro 6 (Wavemetrics) was used for analysis.

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